

WEST Search History

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DATE: Tuesday, September 20, 2005

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
	<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ</i>		
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END OF SEARCH HISTORY

us-10-653-681b-1.Oligo.rng

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 12:07:39 ; Search time 698 Seconds
(without alignments)
9244.295 Million cell updates/sec

Title: US-10-653-681B-1
Perfect score: 1090
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: geneseqn2001as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	780	71.6	1337	5	AAS68608	Aas68608 DNA encod
2	780	71.6	1337	10	ADD71032	Add71032 Human ald
3	773	70.9	1549	12	ADK70274	Adk70274 Respirato
4	729	66.9	1508	3	AAC98140	Aac98140 Human col
5	729	66.9	1560	12	ADJ75119	Adj75119 Marker ge
6	729	66.9	1560	12	ADN04246	Adn04246 Antipsori
7	729	66.9	1560	13	ACN38728	Acn38728 Tumour-as
8	729	66.9	1560	13	ADS85007	Ads85007 Human ato
9	664	60.9	1316	5	AAF68405	Aaf68405 Human lun
10	664	60.9	1316	6	ABK38316	Abk38316 cDNA enco

us-10-653-681b-1.01igo.rng

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	20	328	30.1	364	4	AAS39335	Aas39335 Novel hum
	21	316	29.0	585	2	AAZ24592	Aaz24592 Human lun
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	27	316	29.0	585	10	ADH36746	Adh36746 Human lun
	28	316	29.0	585	12	ADM56549	Adm56549 Human lun
	29	316	29.0	585	12	ADN89593	Adn89593 Human lun
c	30	316	29.0	857	9	ADA28650	Ada28650 Human lun
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c	32	316	29.0	858	3	AAC65830	Aac65830 Human lun
c	33	316	29.0	858	6	ABL49049	Ab149049 Human lun
c	34	316	29.0	858	6	ABQ92235	Abq92235 Human lun
c	35	316	29.0	858	10	ADE53610	Ade53610 Human lun
c	36	316	29.0	858	10	ADH36745	Adh36745 Human lun
c	37	316	29.0	858	12	ADM56548	Adm56548 Human lun
c	38	316	29.0	858	12	ADN89592	Adn89592 Human lun
	39	304	27.9	356	4	AAS39333	Aas39333 Novel hum
	40	252	23.1	1396	5	AAS91091	Aas91091 DNA encod
	41	249	22.8	861	5	AAS68606	Aas68606 DNA encod
	42	235	21.6	830	4	AAI92428	Aai92428 Human pol
	43	183	16.8	540	12	ADP28822	Adp28822 Human sec
	44	174	16.0	857	13	ADR98738	Adr98738 Lung spec
c	45	159	14.6	198	12	ACH84956	Ach84956 Human gen

RESULT 9

AAF68405

ID AAF68405 standard; cDNA; 1316 BP.

XX

AC AAF68405;

XX

DT 12-APR-2001 (first entry)

XX

DE Human lung tumour protein related nucleotide sequence SEQ ID NO:323.

XX

KW Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
cytostatic; antisense inhibition; ss.

XX

OS Homo sapiens.

XX

PN WO200100828-A2.

XX

PD 04-JAN-2001.

XX

PF 30-JUN-2000; 2000WO-US018061.

XX

PR 30-JUN-1999; 99US-00346492.

PR 15-OCT-1999; 99US-00419356.

PR 17-DEC-1999; 99US-00466867.

PR 30-DEC-1999; 99US-00476300.

PR 06-MAR-2000; 2000US-00519642.
 PR 22-MAR-2000; 2000US-00533077.
 PR 10-APR-2000; 2000US-00546259.
 PR 27-APR-2000; 2000US-00560406.
 PR 05-JUN-2000; 2000US-00589184.

XX
 PA (CORI-) CORIXA CORP.

XX
 PI Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
 PI Retter MW, Mannion J;

XX
 DR WPI; 2001-071488/08.

XX
 PT Lung tumor-associated proteins and the nucleic acids that encode them,
 PT useful for preventing, diagnosing and treating lung cancer.

XX
 PS Example 1; Page 249-250; 436pp; English.

XX
 CC The present invention describes immunogenic portions of lung tumour-
 CC associated proteins (I) and the nucleic acids (NAS) that encode them. (I)
 CC have cytostatic activity and can be used in gene therapy, antisense
 CC inhibition and in vaccines. The NAS and the lung tumour-associated
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with their inappropriate expression,
 CC especially lung cancers. For example, the NAS may be administered to
 CC treat diseases by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of the protein by expressing inactive proteins
 CC or to supplement the patients own production of (I). Additionally, the
 CC NAS may be used to produce the lung-tumour associated protein, according
 CC to standard recombinant DNA methodology. Conversely, antisense NA
 CC molecules may be administered to down regulate protein expression by
 CC binding with the cells own genes and preventing their expression. The NA
 CC and complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar NA sequences in
 CC samples, and hence which patients may be in need of treatment for lung
 CC cancer. The (I) may be used as antigens in the production of antibodies
 CC and in assays to identify modulators (agonists and antagonists) of the
 CC expression and activity of the protein. AAF68083 to AAF68878 and AAB76848
 CC to AAB76878 represent human lung tumour protein related nucleotide and
 CC protein sequences which are used in the exemplification of the present
 CC invention

XX
 SQ Sequence 1316 BP; 385 A; 299 C; 308 G; 324 T; 0 U; 0 Other;

Query Match 60.9%; Score 664; DB 5; Length 1316;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 764; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy	371	CCAGGTTGAGTGTACCCATACCTCACGCAGGAGAACTGATCCAGTACTGCCACTCCAA	430
Db	588	CCAGGTTGAGTGTACCCATACCTCACACAGGAGAACTGATCCAGTACTGCCACTCCAA	647
Qy	431	GGGCATCACCGTTACGGCCTACAGCCCCCTGGGCTCTCCGGATAGACCTTGGGCCAAGCC	490
Db	648	GGGCATCACCGTTACGGCCTACAGCCCCCTGGGCTCTCCGGATAGACCTTGGGCCAAGCC	707
Qy	491	AGAAGACCCTTCCCTGCTGGAGGATCCCAAGATTAAGGAGATTGCTGCAAAGCACAAAAA	550
Db	708	AGAAGACCCTTCCCTGCTGGAGGATCCCAAGATTAAGGAGATTGCTGCAAAGCACAAAAA	767

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QY      611 GTCTGTGACACCAGCACGCATTGTTGAGAACATTACAGGTCTTTGACTTTAAATTGAGTGA 670
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Db      828 GTCTGTGACACCAGCACGCATTGTTGAGAACATTACAGGTCTTTGACTTTAAATTGAGTGA 887
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QY      731 ATCCTCTCATTTGGAAGACTATCCCTTCGATGCAGAATATTGAGGTTGAATCTCCTGGTG 790
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Db     1128 TGCTGTTTTAGACATTTATTTCTGTATGTTCAACTAGGATCAGAATATCACAGAAAAGCA 1187
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QY      971 TGGCTTGAATAAGGAAATGACAATTTTTTCCACTTATCTGATCAGAACAAATGTTTATTA 1030
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Db     1188 TGGCTTGAATAAGGAAATGACAATTTTTTCCACTTATCTGATCAGAACAAATGTTTATTA 1247
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QY     1031 AGCATCAGAAACTCTGCCAACACTGAGGATGTAAAGATCAATAAAA 1076
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Db     1248 AGCATCAGAAACTCTGCCAACACTGAGGATGTAAAGATCAATAAAA 1293
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RESULT 10

ABK38316

ID ABK38316 standard; cDNA; 1316 BP.

XX

AC ABK38316;

XX

DT 21-MAY-2002 (first entry)

XX

DE cDNA encoding clone #18973 (L516S) of lung tumour protein.

XX

KW Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
gene; ss.

XX

OS Homo sapiens.

XX

PN WO200204514-A2.

XX

PD 17-JAN-2002.

XX

PF 10-JUL-2001; 2001WO-US022058.

XX

PR 11-JUL-2000; 2000US-00614124.

PR 29-AUG-2000; 2000US-00651563.

PR 08-SEP-2000; 2000US-00658824.

PR 26-SEP-2000; 2000US-00671325.

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PR      06-OCT-2000; 2000US-00677419.  
PR      30-OCT-2000; 2000US-00702705.  
PR      13-DEC-2000; 2000US-00736457.  
PR      03-MAY-2001; 2001US-00849626.  
XX  
PA      (CORI-) CORIXA CORP.  
XX  
PI      Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;  
PI      Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS, McNabb A;  
PI      Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;  
XX  
DR      WPI; 2002-164634/21.  
XX  
PT      Novel polynucleotide encoding a lung tumor polypeptide useful for  
PT      stimulating and/or expanding T cells specific for a tumor protein.  
XX  
PS      Example 1; SEQ ID NO 323; 223pp; English.  
XX  
CC      The invention describes an isolated polynucleotide and polypeptide useful  
CC      for stimulating and/or expanding T cells specific for a tumour protein  
CC      for determining the presence of a cancer in a patient. A composition  
CC      containing the polynucleotide and/or polypeptide is useful for treating a  
CC      lung cancer in a patient. The polypeptide is useful for removing tumour  
CC      cells from a biological sample. The polynucleotide is also useful as  
CC      probe or primer to detect the level of mRNA encoding a tumour protein.  
CC      This sequence encodes a lung tumour associated protein or protein  
CC      fragment, described in the method of the invention. Note: The sequence  
CC      data for this patent did not form part of the printed specification, but  
CC      was obtained in electronic format directly from WIPO at  
CC      ftp.wipo.int/pub/published_pct_sequences  
XX  
SQ      Sequence 1316 BP; 385 A; 299 C; 308 G; 324 T; 0 U; 0 Other;  
  
Query Match          60.9%; Score 664; DB 6; Length 1316;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 764; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db	948	ATCCTCTCATTTGGAAGACTATCCCTTCAATGCAGAATATTGAGGTTGAATCTCCTGGTG	1007
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Qy	911	TGCTGTTTTAGACATTTATTTCTGTATGTTCAACTAGGATCAGAATATCACAGAAAAGCA	970
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Qy	1031	AGCATCAGAAACTCTGCCAACACTGAGGATGTAAAGATCAATAAAA	1076
Db	1248	AGCATCAGAAACTCTGCCAACACTGAGGATGTAAAGATCAATAAAA	1293

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 11:49:49 ; Search time 5147 Seconds
(without alignments)
10261.548 Million cell updates/sec

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 9416466

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Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	664	60.9	1316	6	AR406467	AR406467	Sequence
9	664	60.9	1316	6	AR440317	AR440317	Sequence
10	664	60.9	1316	6	AR472475	AR472475	Sequence
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17	410	37.6	951	12	BT007750	BT007750	Synthetic
18	409	37.5	948	9	CR541801	CR541801	Homo sapi
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ALIGNMENTS

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 ACCESSION CQ718316
 VERSION CQ718316.1 GI:42279173
 KEYWORDS .

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
 TITLE Kits, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof
 JOURNAL Patent: WO 02068579-A 4250 06-SEP-2002;
 PE Corporation (NY) (US)
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 /db_xref="taxon:9606"

ORIGIN

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 0;

Qy 311 CCACTTCCAGATCGAGAAGCTCTTGAACAAACCTGGACTGAAATATAAACAGTGACTAA 370
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 Db 677 GGGCATCACCGTTACGGCCTACAGCCCCCTGGGCTCTCCGGATAGACCTTGGGCCAAGCC 736
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 Qy 611 GTCTGTGACACCAGCACGCATTGTTGAGAACATTTCAGGTCTTTGACTTTAAATTGAGTGA 670
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1090			
Db	1277	AGCATCAGAAACTCTGCCAACACTGAGGATGTAAAGATCAATAAAAAAAAAATAATAATCAT	
1336			

us-10-653-681b-1.Oligo.rng

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 12:07:39 ; Search time 698 Seconds
(without alignments)
9244.295 Million cell updates/sec

Title: US-10-653-681B-1
Perfect score: 1090
Sequence: 1 caaaaacagcaacagaaagc.....ataaaaaaaataataatcat 1090

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	780	71.6	1337	5 AAS68608	Aas68608 DNA encod
2	780	71.6	1337	10 ADD71032	Add71032 Human ald
3	773	70.9	1549	12 ADK70274	Adk70274 Respirato
4	729	66.9	1508	3 AAC98140	Aac98140 Human col
5	729	66.9	1560	12 ADJ75119	Adj75119 Marker ge
6	729	66.9	1560	12 ADN04246	Adn04246 Antipsori
7	729	66.9	1560	13 ACN38728	Acn38728 Tumour-as
8	729	66.9	1560	13 ADS85007	Ads85007 Human ato
9	664	60.9	1316	5 AAF68405	Aaf68405 Human lun
10	664	60.9	1316	6 ABK38316	Abk38316 cDNA enco

us-10-653-681b-1.Oligo.rng										
	11	664	60.9	1316	7	ADS73134	Ads73134	Human	kid	
	12	664	60.9	1316	8	ACA10645	Aca10645	Human	lun	
	13	664	60.9	1316	8	ABX99596	Abx99596	Lung	canc	
	14	664	60.9	1316	10	ADH45842	Adh45842	Human	lun	
	15	664	60.9	1316	12	ADE72379	Ade72379	Human	lun	
	16	664	60.9	1316	13	ADJ19761	Adj19761	Human	lun	
	17	529	48.5	770	13	ADR98739	Adr98739	Lung	spec	
	18	529	48.5	1621	12	ADH13722	Adh13722	Human	ENZ	
c	19	389	35.7	558	10	ABZ84625	Abz84625	Toxicolog		
	20	328	30.1	364	4	AAS39335	Aas39335	Novel	hum	
	21	316	29.0	585	2	AAZ24592	Aaz24592	Human	lun	
	22	316	29.0	585	3	AAC65831	Aac65831	Human	lun	
	23	316	29.0	585	6	ABL49050	Ab149050	Human	lun	
	24	316	29.0	585	6	ABQ92236	Abq92236	Human	lun	
	25	316	29.0	585	9	ADA28651	Ada28651	Human	lun	
	26	316	29.0	585	10	ADE53611	Ade53611	Human	lun	
	27	316	29.0	585	10	ADH36746	Adh36746	Human	lun	
	28	316	29.0	585	12	ADM56549	Adm56549	Human	lun	
	29	316	29.0	585	12	ADN89593	Adn89593	Human	lun	
c	30	316	29.0	857	9	ADA28650	Ada28650	Human	lun	
c	31	316	29.0	858	2	AAZ24591	Aaz24591	Human	lun	
c	32	316	29.0	858	3	AAC65830	Aac65830	Human	lun	
c	33	316	29.0	858	6	ABL49049	Ab149049	Human	lun	
c	34	316	29.0	858	6	ABQ92235	Abq92235	Human	lun	
c	35	316	29.0	858	10	ADE53610	Ade53610	Human	lun	
c	36	316	29.0	858	10	ADH36745	Adh36745	Human	lun	
c	37	316	29.0	858	12	ADM56548	Adm56548	Human	lun	
c	38	316	29.0	858	12	ADN89592	Adn89592	Human	lun	
	39	304	27.9	356	4	AAS39333	Aas39333	Novel	hum	
	40	252	23.1	1396	5	AAS91091	Aas91091	DNA	encod	
	41	249	22.8	861	5	AAS68606	Aas68606	DNA	encod	
	42	235	21.6	830	4	AAI92428	Aai92428	Human	pol	
	43	183	16.8	540	12	ADP28822	Adp28822	Human	sec	
	44	174	16.0	857	13	ADR98738	Adr98738	Lung	spec	
c	45	159	14.6	198	12	ACH84956	Ach84956	Human	gen	

ALIGNMENTS

RESULT 1

AAS68608

ID AAS68608 standard; cDNA; 1337 BP.

XX

AC AAS68608;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #4412.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

Sequence 1337 BP; 390 A; 305 C; 318 G; 324 T; 0 U; 0 other:

Query Match 71.6%; Score 780; DB 5; Length 1337;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Page 3

us-10-653-681b-1.Oligo.rng

Qy	611	GTCTGTGACACCAGCACGCATTGTTGAGAACATTTCAGGTCTTTGACTTTAAATTGAGTGA	670
Db	858	GTCTGTGACACCAGCACGCATTGTTGAGAACATTTCAGGTCTTTGACTTTAAATTGAGTGA	917
Qy	671	TGAGGAGATGGCAACCATACTCAGCTTCAACAGAACTGGAGGGCCTGTAACGTGTTGCA	730
Db	918	TGAGGAGATGGCAACCATACTCAGCTTCAACAGAACTGGAGGGCCTGTAACGTGTTGCA	977
Qy	731	ATCCTCTCATTTGGAAGACTATCCCTTCGATGCAGAATATTGAGGTTGAATCTCCTGGTG	790
Db	978	ATCCTCTCATTTGGAAGACTATCCCTTCGATGCAGAATATTGAGGTTGAATCTCCTGGTG	1037
Qy	791	AGATTATACAGGAGATTCTCTTTCTTCGCTGAAGTGTGACTACCTCCACTCATGTCCCAT	850
Db	1038	AGATTATACAGGAGATTCTCTTTCTTCGCTGAAGTGTGACTACCTCCACTCATGTCCCAT	1097
Qy	851	TTTAGCCAAGCTTATTTAAGATCACAGTGAACCTAGTCCTGTTATAGACGAGAATCGAGG	910
Db	1098	TTTAGCCAAGCTTATTTAAGATCACAGTGAACCTAGTCCTGTTATAGACGAGAATCGAGG	1157
Qy	911	TGCTGTTTTAGACATTTATTTCTGTATGTTCAACTAGGATCAGAATATCACAGAAAAGCA	970
Db	1158	TGCTGTTTTAGACATTTATTTCTGTATGTTCAACTAGGATCAGAATATCACAGAAAAGCA	1217
Qy	971	TGGCTTGAATAAGGAAATGACAATTTTTTCCACTTATCTGATCAGAACAAATGTTTATTA	1030
Db	1218	TGGCTTGAATAAGGAAATGACAATTTTTTCCACTTATCTGATCAGAACAAATGTTTATTA	1277
Qy	1031	AGCATCAGAACTCTGCCAACACTGAGGATGTAAAGATCAATAAAAAAAAAATAATCAT	1090
Db	1278	AGCATCAGAACTCTGCCAACACTGAGGATGTAAAGATCAATAAAAAAAAAATAATCAT	1337

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 11:53:34 ; Search time 4250 Seconds
(without alignments)
9762.366 Million cell updates/sec

Title: US-10-653-681B-1
Perfect score: 1090
Sequence: 1 caaaaacagcaacagaaagc.....ataaaaaaataataatcat 1090

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		ID	Description
	No.	Score	Match	Length	DB	ID		
c	1	629	57.7	735	5	BM981698	BM981698	UI-CF-EN1
	2	585	53.7	613	6	CB132708	CB132708	K-EST0183
c	3	570	52.3	593	5	BU677104	BU677104	UI-CF-DU1
	4	517	47.4	588	2	BE785963	BE785963	601478213
c	5	496	45.5	540	1	AA804597	AA804597	nk97e06.s
	6	493	45.2	623	4	BM793014	BM793014	K-EST0073
c	7	479	43.9	595	5	BM983180	BM983180	UI-CF-EN1
c	8	454	41.7	644	6	CA450136	CA450136	UI-CF-FN0

c	9	446	40.9	456	1	AI292337	AI292337	qm77c02.x
c	10	446	40.9	458	1	AI744504	AI744504	wg09a09.x
c	11	446	40.9	460	1	AI291463	AI291463	qm73h04.x
c	12	444	40.7	452	1	AI393702	AI393702	tg66d01.x
c	13	432	39.6	446	5	BX104876	BX104876	BX104876
	14	431	39.5	592	4	BM819663	BM819663	K-EST0087
c	15	426	39.1	448	5	BM975664	BM975664	UI-CF-EN1
	16	417	38.3	445	6	CB161124	CB161124	K-EST0220
	17	401	36.8	635	7	CV334625	CV334625	IL3-UT011
	18	400	36.7	620	6	CB118695	CB118695	K-EST0165
c	19	392	36.0	746	2	BF688991	BF688991	602185236
	20	385	35.3	453	4	BG197874	BG197874	RST17122
c	21	378	34.7	388	1	AI831519	AI831519	wj49h11.x
c	22	363	33.3	445	1	AI301329	AI301329	qn27e09.x
c	23	363	33.3	496	2	AW379341	AW379341	MRO-HT024
	24	361	33.1	384	2	BE787870	BE787870	601479812
	25	360	33.0	796	4	BG682196	BG682196	602629503
c	26	345	31.7	388	2	BE711936	BE711936	QV2-HT069
	27	341	31.3	485	7	CV334678	CV334678	IL3-UT011
c	28	338	31.0	415	1	AA947514	AA947514	oq53h01.s
	29	329	30.2	786	5	BQ221381	BQ221381	AGENCOURT
	30	324	29.7	365	5	BQ377471	BQ377471	IL2-UM007
	31	319	29.3	319	4	BM855292	BM855292	K-EST0138
	32	316	29.0	729	5	BX480365	BX480365	DKFZp6860
	33	316	29.0	1177	4	BM558121	BM558121	AGENCOURT
c	34	314	28.8	666	1	AI924753	AI924753	wn58a02.x
c	35	300	27.5	300	1	AI270664	AI270664	qu90c04.x
c	36	299	27.4	549	5	BQ315282	BQ315282	RC3-IT001
	37	299	27.4	909	4	BG169378	BG169378	602320937
	38	296	27.2	316	5	BU175462	BU175462	AGENCOURT
	39	295	27.1	310	4	BM783186	BM783186	K-EST0061
c	40	292	26.8	346	2	BE775022	BE775022	IL2-UM007
	41	285	26.1	582	5	BP278752	BP278752	BP278752
	42	280	25.7	581	5	BP263763	BP263763	BP263763
	43	272	25.0	912	5	BQ220848	BQ220848	AGENCOURT
	44	248	22.8	535	6	CB147729	CB147729	K-EST0203
	45	248	22.8	557	4	BG490449	BG490449	602519494

ALIGNMENTS

RESULT 1

BM981698/c

LOCUS BM981698 735 bp mRNA linear EST 21-FEB-2003

DEFINITION UI-CF-EN1-adi-f-17-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
UI-CF-EN1-adi-f-17-0-UI 3', mRNA sequence.

ACCESSION BM981698

VERSION BM981698.1 GI:19604453

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 735)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-44, >POLY_A#Simple_repeat (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .735
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-adi-f-17-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 57.7%; Score 629; DB 5; Length 735;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	462	GGCTCTCCGGATAGACCTTGGGCCAAGCCAGAAGACCCTTCCCTGCTGGAGGATCCCAAG	521
Db	645	GGCTCTCCGGATAGACCTTGGGCCAAGCCAGAAGACCCTTCCCTGCTGGAGGATCCCAAG	586
Qy	522	ATTAAGGAGATTGCTGCAAAGCACAAAAAACCGCAGCCCAGGTTCTGATCCGTTTCCAT	581
Db	585	ATTAAGGAGATTGCTGCAAAGCACAAAAAACCGCAGCCCAGGTTCTGATCCGTTTCCAT	526
Qy	582	ATCCAGAGGAATGTGATTGTCATCCCCAAGTCTGTGACACCAGCACGCATTGTTGAGAAC	641
Db	525	ATCCAGAGGAATGTGATTGTCATCCCCAAGTCTGTGACACCAGCACGCATTGTTGAGAAC	466
Qy	642	ATTCAGGTCTTTGACTTTAAATTGAGTGATGAGGAGATGGCAACCATACTCAGCTTCAAC	701
Db	465	ATTCAGGTCTTTGACTTTAAATTGAGTGATGAGGAGATGGCAACCATACTCAGCTTCAAC	406
Qy	702	AGAAACTGGAGGGCCTGTAACGTGTTGCAATCCTCTCATTTGGAAGACTATCCCTTCGAT	761
Db	405	AGAAACTGGAGGGCCTGTAACGTGTTGCAATCCTCTCATTTGGAAGACTATCCCTTCGAT	346
Qy	762	GCAGAAATATTGAGGTTGAATCTCCTGGTGAGATTATACAGGAGATTCTCTTTCTTCGCTG	821
Db	345	GCAGAAATATTGAGGTTGAATCTCCTGGTGAGATTATACAGGAGATTCTCTTTCTTCGCTG	286
Qy	822	AAGTGTGACTACCTCCACTCATGTCCCATTTTAGCCAAGCTTATTTAAGATCACAGTGAA	881
Db	285	AAGTGTGACTACCTCCACTCATGTCCCATTTTAGCCAAGCTTATTTAAGATCACAGTGAA	226
Qy	882	CTTAGTCCTGTTATAGACGAGAATCGAGGTGCTGTTTTAGACATTTATTTCTGTATGTTT	941
Db	225	CTTAGTCCTGTTATAGACGAGAATCGAGGTGCTGTTTTAGACATTTATTTCTGTATGTTT	166
Qy	942	AACTAGGATCAGAAATATCACAGAAAAGCATGGCTTGAATAAGGAAATGACAATTTTTTCC	1001
Db	165	AACTAGGATCAGAAATATCACAGAAAAGCATGGCTTGAATAAGGAAATGACAATTTTTTCC	106
Qy	1002	ACTTATCTGATCAGAACAAATGTTTATTAAGCATCAGAAACTCTGCCAACACTGAGGATG	1061
Db	105	ACTTATCTGATCAGAACAAATGTTTATTAAGCATCAGAAACTCTGCCAACACTGAGGATG	46
Qy	1062	TAAAGATCAATAAAAAAAAAATAAATCAT	1090
Db	45	TAAAGATCAATAAAAAAAAAATAAATCAT	17

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 06:02:48 ; Search time 5146 Seconds
(without alignments)
10263.542 Million cell updates/sec

Title: US-10-653-681B-1
Perfect score: 1090
Sequence: 1 caaaaacagcaacagaaagc.....ataaaaaaaataataatcat 1090

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	833	76.4	1337	9	HSU37100	U37100 Homo sapien
2	830.8	76.2	1336	6	CQ718316	CQ718316 Sequence

3	828.2	76.0	1551	9	BC008837	BC008837 Homo sapi
4	828.2	76.0	1560	6	CQ776685	CQ776685 Sequence
5	820.2	75.2	1611	9	AF524864	AF524864 Homo sapi
6	796.6	73.1	1316	6	AR272611	AR272611 Sequence
7	796.6	73.1	1316	6	AR276192	AR276192 Sequence
8	796.6	73.1	1316	6	AR406467	AR406467 Sequence
9	796.6	73.1	1316	6	AR440317	AR440317 Sequence
10	796.6	73.1	1316	6	AR472475	AR472475 Sequence
11	796.6	73.1	1316	6	AR543128	AR543128 Sequence
12	796.6	73.1	1316	6	AX062696	AX062696 Sequence
13	796.6	73.1	1316	6	AX367613	AX367613 Sequence
14	796.6	73.1	1316	9	AF052577	AF052577 Homo sapi
15	718.	65.9	1315	6	AX743782	AX743782 Sequence
16	651.8	59.8	3994	9	AL669847	AL669847 Human DNA
17	651.8	59.8	121210	9	AL607022	AL607022 Human DNA
18	574	52.7	574	9	AF044961	AF044961 Homo sapi
19	508	46.6	1080	6	AX772965	AX772965 Sequence
20	459.4	42.1	951	9	BT006794	BT006794 Homo sapi
21	459.4	42.1	951	12	BT007750	BT007750 Synthetic
22	458.4	42.1	948	9	CR541801	CR541801 Homo sapi
23	431	39.5	951	6	AX380448	AX380448 Sequence
24	431	39.5	951	6	AX772962	AX772962 Sequence
25	395.6	36.3	473	9	AY347931	AY347931 Macaca ra
26	377.8	34.7	144234	2	AP002425	AP002425 Homo sapi
c 27	377.8	34.7	144279	2	AP001570	AP001570 Homo sapi
c 28	377.8	34.7	216972	9	AC067819	AC067819 Homo sapi
29	374.8	34.4	585	6	CQ732993	CQ732993 Sequence
c 30	361	33.1	137557	9	AC005909	AC005909 Homo sapi
31	360.4	33.1	364	6	AX247463	AX247463 Sequence
32	358.4	32.9	163631	9	AC009276	AC009276 Homo sapi
c 33	358.4	32.9	170919	9	AC078847	AC078847 Homo sapi
c 34	358.4	32.9	177373	2	AP002452	AP002452 Homo sapi
35	358.4	32.9	196039	2	AC055757	AC055757 Homo sapi
36	357.2	32.8	1268	10	CGU81045	U81045 Cricetulus
37	354.4	32.5	1400	10	BC037690	BC037690 Mus muscu
38	353.4	32.4	356	6	AX247461	AX247461 Sequence
39	353.4	32.4	1446	10	BC079133	BC079133 Rattus no
40	344.6	31.6	1413	10	AF182168	AF182168 Rattus no
41	332	30.5	1315	10	BC005789	BC005789 Mus muscu
42	331.6	30.4	1304	10	MMU04204	U04204 Mus musculu
43	327.2	30.0	1225	6	CQ777549	CQ777549 Sequence
44	327.2	30.0	1225	10	MUSMVP	J05663 Mouse vas d
45	327	30.0	993	10	RNO277957	AJ277957 Rattus no

ALIGNMENTS

RESULT 1
 HSU37100
 LOCUS HSU37100 1337 bp mRNA linear PRI 28-MAY-1998
 DEFINITION Homo sapiens aldose reductase-like peptide mRNA, complete cds.
 ACCESSION U37100
 VERSION U37100.1 GI:3150034
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1337)
 AUTHORS Cao,D., Fan,S.T. and Chung,S.S.
 TITLE Identification and characterization of a novel human aldose
 reductase-like gene
 JOURNAL J. Biol. Chem. 273 (19), 11429-11435 (1998)
 MEDLINE 98234319
 PUBMED 9565553
 REFERENCE 2 (bases 1 to 1337)
 AUTHORS Cao,D.
 TITLE Direct Submission
 JOURNAL Submitted (27-SEP-1995) Deliang Cao, The University of Hong Kong,
 Institute of Molecular Biology, 8 Sassoon Road, Pokfulam, Hong
 Kong, Hong Kong

FEATURES Location/Qualifiers
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ORIGIN

Query Match 76.4%; Score 833; DB 9; Length 1337;
 Best Local Similarity 81.5%; Pred. No. 1.4e-221;
 Matches 1090; Conservative 0; Mismatches 0; Indels 247; Gaps

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us-10-653-681b-1.rng

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Run on: August 9, 2005, 05:31:49 ; Search time 697 Seconds
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9257.558 Million cell updates/sec

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Searched: 4390206 seqs, 2959870667 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	828.2	76.0	1560	13	ADS85007	Ads85007 Human ato
8	822.8	75.5	1549	12	ADK70274	Adk70274 Respirato
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10	796.6	73.1	1316	6	ABK38316	Abk38316 cDNA enco

us-10-653-681b-1.rng							
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13	796.6	73.1	1316	8	ABX99596	Abx99596	Lung canc
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18	718	65.9	1315	10	ADC97771	Adc97771	Human ARL
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20	616	56.5	770	13	ADR98739	Adr98739	Lung spec
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ALIGNMENTS

RESULT 1

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ID AAS68608 standard; cDNA; 1337 BP.

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AC AAS68608;

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DT 13-FEB-2002 (first entry)

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DE DNA encoding novel human diagnostic protein #4412.

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KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

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OS Homo sapiens.

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PN WO200175067-A2.

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PD 11-OCT-2001.

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PF 30-MAR-2001; 2001WO-US008631.

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PR 23-AUG-2000; 2000US-00649167.

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(HYSE-) HYSEQ INC.

Drmanac RT, Liu C, Tang YT;

WPI; 2001-639362/73.

P-PSDB; ABG04421.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 4412; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](ftp:wipo.int/pub/published_pct_sequences)

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us-10-653-681b-1.rng

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	729	66.9	1515	4	US-09-949-016-1344	Sequence 1344, Ap
2	664	60.9	1316	4	US-09-702-705-323	Sequence 323, App
3	664	60.9	1316	4	US-09-736-457-323	Sequence 323, App
4	664	60.9	1316	4	US-09-614-124B-323	Sequence 323, App
5	664	60.9	1316	4	US-09-671-325-323	Sequence 323, App
6	664	60.9	1316	4	US-09-589-184-323	Sequence 323, App
7	664	60.9	1316	4	US-09-658-824-323	Sequence 323, App
8	331	30.4	17740	4	US-09-949-016-13086	Sequence 13086, A
9	316	29.0	585	3	US-09-123-912-92	Sequence 92, Appl
10	316	29.0	585	3	US-09-643-597-92	Sequence 92, Appl
11	316	29.0	585	4	US-09-480-884A-92	Sequence 92, Appl
12	316	29.0	585	4	US-09-542-615A-92	Sequence 92, Appl
13	316	29.0	585	4	US-09-606-421B-92	Sequence 92, Appl
14	316	29.0	585	4	US-09-221-107-92	Sequence 92, Appl
15	316	29.0	585	4	US-09-466-396A-92	Sequence 92, Appl
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					us-10-653-681b-1.oligo.rni	
	18	316	29.0	585	4	US-09-285-479-92 Sequence 92, Appl
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ALIGNMENTS

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; Sequence 1344, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1344

; LENGTH: 1515

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-1344

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 Best Local Similarity 99.9%; Pred. No. 0;
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us-10-653-681b-1.Oligo.rni

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	664	60.9	1316	9	US-09-736-457-323	Sequence 323, App
5	664	60.9	1316	9	US-09-902-941-323	Sequence 323, App
6	664	60.9	1316	9	US-09-849-626-323	Sequence 323, App
7	664	60.9	1316	10	US-09-476-300-323	Sequence 323, App
8	664	60.9	1316	14	US-10-017-754-323	Sequence 323, App
9	664	60.9	1316	15	US-10-102-524-1731	Sequence 1731, Ap
10	664	60.9	1316	16	US-10-113-872-323	Sequence 323, App
11	664	60.9	1316	17	US-10-283-017-323	Sequence 323, App
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13	328	30.1	364	10	US-09-803-719-2393	Sequence 2393, Ap
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15	316	29.0	585	9	US-09-850-716A-92	Sequence 92, Appl
16	316	29.0	585	9	US-09-897-778-92	Sequence 92, Appl
17	316	29.0	585	10	US-09-466-396A-92	Sequence 92, Appl
18	316	29.0	585	14	US-10-007-700-92	Sequence 92, Appl
19	316	29.0	585	15	US-10-117-982-92	Sequence 92, Appl
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C 25	316	29.0	858	9	US-09-897-778-91	Sequence 91, Appl
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C 27	316	29.0	858	14	US-10-007-700-91	Sequence 91, Appl
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38	144	13.2	233	9	US-09-736-457-31	Sequence 31, Appl
39	144	13.2	233	9	US-09-902-941-31	Sequence 31, Appl
40	144	13.2	233	9	US-09-849-626-31	Sequence 31, Appl
41	144	13.2	233	10	US-09-476-300-31	Sequence 31, Appl
42	144	13.2	233	14	US-10-017-754-31	Sequence 31, Appl
43	144	13.2	233	16	US-10-113-872-31	Sequence 31, Appl
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45	116	10.6	1816	14	US-10-198-846-14071	Sequence 14071, A

ALIGNMENTS

RESULT 1

US-10-653-681A-1

; Sequence 1, Application US/10653681A

; Publication No. US20050048503A1

; GENERAL INFORMATION:

; APPLICANT: DAI, KEN-SHOW

; TITLE OF INVENTION: HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER

; FILE REFERENCE: U014798-3

; CURRENT APPLICATION NUMBER: US/10/653,681A

; CURRENT FILING DATE: 2003-09-02

us-10-653-681b-1.oligo.rnpb

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; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)..(333)
US-10-653-681A-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	796.6	73.1	1316	4	US-09-671-325-323 Sequence 323, App
6	796.6	73.1	1316	4	US-09-589-184-323 Sequence 323, App
7	796.6	73.1	1316	4	US-09-658-824-323 Sequence 323, App
8	389.2	35.7	914	4	US-09-949-016-3127 Sequence 3127, Ap
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17	316	29.0	585	4	US-09-466-396A-92 Sequence 92, Appl

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c	26	316	29.0	858	4	US-09-221-107-91	Sequence 91, Appl
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ALIGNMENTS

RESULT 1

US-09-949-016-1344

; Sequence 1344, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1344

; LENGTH: 1515

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-1344

Query Match 76.0%; Score 828.2; DB 4; Length 1515;
 Best Local Similarity 81.3%; Pred. No. 1.2e-247;
 Matches 1087; Conservative 0; Mismatches 3; Indels 247; Gaps 1;

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Qy	121		CTGGGCACTTGGAAGTCTCCTCTCGGCAAAGTGAAAGAAGCAGTGAAGGTGGCCATTGAT	180
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Qy	181		GCAGGATATCGGCACATTGACTGTGCCTATGTCTATCAGAATGAACATGAAGTGGGGGAA	240
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	796.6	73.1	1316	9	US-09-902-941-323	Sequence 323, App
6	796.6	73.1	1316	9	US-09-849-626-323	Sequence 323, App
7	796.6	73.1	1316	10	US-09-476-300-323	Sequence 323, App
8	796.6	73.1	1316	14	US-10-017-754-323	Sequence 323, App
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13	707	64.9	1279	21	US-10-653-681A-3	Sequence 3, Appli
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23	316	29.0	585	14	US-10-007-700-92	Sequence 92, Appl
24	316	29.0	585	15	US-10-117-982-92	Sequence 92, Appl
25	316	29.0	585	17	US-10-313-986-92	Sequence 92, Appl
26	316	29.0	585	20	US-10-775-972-92	Sequence 92, Appl
27	316	29.0	585	22	US-10-922-124-92	Sequence 92, Appl
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C 33	316	29.0	858	15	US-10-117-982-91	Sequence 91, Appl
C 34	316	29.0	858	17	US-10-313-986-91	Sequence 91, Appl
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40	304.8	28.0	1367	15	US-10-171-581-1	Sequence 1, Appli
41	304.8	28.0	1367	17	US-10-172-118-641	Sequence 641, App
42	304.8	28.0	1367	18	US-10-342-887-641	Sequence 641, App
43	304.8	28.0	1367	19	US-10-717-597-289	Sequence 289, App
44	304.8	28.0	1368	19	US-10-416-330-21	Sequence 21, Appl
45	304.8	28.0	1416	21	US-10-887-553A-128	Sequence 128, App

ALIGNMENTS

RESULT 1

US-10-653-681A-1

; Sequence 1, Application US/10653681A

; Publication No. US20050048503A1

; GENERAL INFORMATION:

; APPLICANT: DAI, KEN-SHOW

; TITLE OF INVENTION: HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER

; FILE REFERENCE: U014798-3

; CURRENT APPLICATION NUMBER: US/10/653,681A

; CURRENT FILING DATE: 2003-09-02

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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
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;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE
;   FEATURE:
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;   LOCATION: (70)..(333)
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